## **SEQUENCE LISTING**

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<110> MARBAN, EDUARDO

<120> SOMATIC TRANSFER OF MODIFIED GENES TO PREDICT DRUG EFFECTS

<130> 47728(1699)

<140> 09/187,669

<141> 1998-11-05

<150> 60/064,893

<151> 1997-11-07

<160>2

<170> Patentin Ver. 2.1

<210> 1

<211> 630

<212> PRT

<213> Unknown Organism

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<223> Description of Unknown Organism: Mammalian ion channel protein

<400> 1

Met Ala Ala Gly Val Ala Ala Trp Leu Pro Phe Ala Arg Ala Ala Ala

1

5

Ile Gly Trp Met Pro Val Ala Ser Gly Pro Met Pro Ala Pro Pro Arg

20

25

10

30

15

Gin Giu Arg Lys Arg Thr Gin Asp Ala Leu Ile Val Leu Asn Val Ser

35

40

45

Gly Thr Arg Phe Gln Thr Trp Gln Asp Thr Leu Glu Arg Tyr Pro Asp 50 55 60

Thr Leu Leu Gly Ser Ser Glu Arg Asp Phe Phe Tyr His Pro Glu Thr 65 70 75 80

Gln Gln Tyr Phe Phe Asp Arg Asp Pro Asp Ile Phe Arg His Ile Leu 85 90 95

Asn Phe Tyr Arg Thr Gly Lys Leu His Tyr Pro Arg His Glu Cys lle 100 105 110

Ser Ala Tyr Asp Glu Glu Leu Ala Phe Phe Gly Leu lle Pro Glu lle 115 120 125

lle Gly Asp Cys Cys Tyr Glu Glu Tyr Lys Asp Arg Arg Arg Glu Asn 130 135 140

Ala Glu Arg Leu Gln Asp Asp Ala Asp Thr Asp Asn Thr Gly Glu Ser 145 150 155 160

Ala Leu Pro Thr Met Thr Ala Arg Gln Arg Val Trp Arg Ala Phe Glu 165 170 175

Asn Pro His Thr Ser Thr Met Ala Leu Val Phe Tyr Tyr Val Thr Gly
180 185 190

Phe Phe Ile Ala Val Ser Val Ile Ala Asn Val Val Glu Thr Val Pro 195 200 205

Cys Gly Ser Ser Pro Gly His IIe Lys Glu Leu Pro Cys Gly Glu Arg 210 215 220

Tyr Ala Val Ala Phe Phe Cys Leu Asp Thr Ala Cys Val Met Ile Phe 225 230 235 240

Thr Val Glu Tyr Leu Leu Arg Leu Ala Ala Ala Pro Ser Arg Tyr Arg 245 250 255

Phe Val Arg Ser Val Met Ser IIe IIe Asp Val Val Ala IIe Leu Pro 260 265 270

Tyr Tyr Ile Gly Leu Val Met Thr Asp Asn Glu Asp Val Ser Gly Ala 275 280 285

Phe Val Thr Leu Arg Val Phe Arg Val Phe Arg Ile Phe Lys Phe Ser 290 295 300

Arg His Ser Gly Gly Leu Arg Ile Leu Gly Tyr Thr Leu Lys Ser Cys 305 310 315 320

Ala Ser Glu Leu Gly Phe Leu Leu Phe Ser Leu Thr Met Ala IIe IIe 325 330 335

lle Phe Ala Thr Val Met Phe Tyr Ala Glu Lys Gly Ser Ser Ala Ser 340 345 350

Lys Phe Thr Ser Ile Pro Ala Ala Phe Trp Tyr Thr Ile Val Thr Met 355 360 365

Thr Thr Leu Gly Tyr Gly Asp Met Val Pro Lys Thr Ile Ala Gly Lys 370 375 380

Ile Phe Gly Ser Ile Cys Ser Leu Ser Gly Val Leu Val Ile Ala Leu 385 390 395 400

Pro Val Pro Val Ile Val Ser Asn Phe Ser Arg Ile Tyr His Gln Asn 405 410 415

V

Gln Arg Ala Asp Lys Arg Arg Ala Gln Lys Lys Ala Arg Leu Ala Arg 420 425 430

Ile Arg Ala Ala Lys Ser Gly Ser Ala Asn Ala Tyr Met Gln Ser Lys

435

440

445

Arg Asn Gly Leu Ser Asn Gln Leu Gln Ser Ser Glu Asp Glu Pro 450 455 460

Ala Phe Val Ser Lys Ser Gly Ser Ser Phe Glu Thr Gln His His His 465 470 475 480

Leu Leu His Cys Leu Glu Lys Thr Thr Asn His Glu Phe Val Asp Glu 485 490 495

Gln Val Phe Glu Glu Ser Cys Met Glu Val Ala Thr Val Asn Arg Pro 500 505 510

Ser Ser His Ser Pro Ser Leu Ser Ser Gln Gln Gly Val Thr Ser Thr 515 520 525

Cys Cys Ser Arg Arg His Lys Lys Thr Phe Arg lle Pro Asn Ala Asn 530 535 540

Val Ser Gly Ser His Arg Gly Ser Val Gln Glu Leu Ser Thr Ile Gln 545 550 555 560

Ile Arg Cys Val Glu Arg Thr Pro Leu Ser Asn Ser Arg Ser Ser Leu 565 570 575

Asn Ala Lys Met Glu Glu Cys Val Lys Leu Asn Cys Glu Gln Pro Tyr 580 585 590

Val Thr Thr Ala IIe IIe Ser IIe Pro Thr Pro Pro Val Thr Thr Pro 595 600 605

Glu Gly Asp Asp Arg Pro Glu Ser Pro Glu Tyr Ser Gly Gly Asn Ile 610 615 620

Val Arg Val Ser Ala Leu 625 630

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                       10
                                    15
lle Gly Trp Met Pro Val Ala Ser Gly Pro Met Pro Ala Pro Pro Arg
                     25
                                  30
Gln Glu Arg Lys Arg Thr Gln Asp Ala Leu Ile Val Leu Asn Val Ser
                  40
                               45
Gly Thr Arg Phe Gln Thr Trp Gln Asp Thr Leu Glu Arg Tyr Pro Asp
                55
                             60
Thr Leu Leu Gly Ser Ser Glu Arg Asp Phe Phe Tyr His Pro Glu Thr
65
             70
                           75
                                        80
Gln Gln Tyr Phe Phe Asp Arg Asp Pro Asp Ile Phe Arg His Ile Leu
          85
                       90
                                    95
Asn Phe Tyr Arg Thr Gly Lys Leu His Tyr Pro Arg His Glu Cys Ile
       100
                     105
                                  110
Ser Ala Tyr Asp Glu Glu Leu Ala Phe Phe Gly Leu lle Pro Glu lle
    115
                  120
                                125
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lle Gly Asp Cys Cys Tyr Glu Glu Tyr Lys Asp Arg Arg Arg Glu Asn

Ala Glu Arg Leu Gln Asp Asp Ala Asp Thr Asp Asn Thr Gly Glu Ser

Ala Leu Pro Thr Met Thr Ala Arg Gln Arg Val Trp Arg Ala Phe Glu

Asn Pro His Thr Ser Thr Met Ala Leu Val Phe Tyr Tyr Val Thr Gly

Phe Phe Ile Ala Val Ser Val Ile Ala Asn Val Val Glu Thr Gly Ser

Arg His Asp Lys IIe His